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I-GOST A Phylogenomic Tool For Plant Comparative Genomics

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I-GOST (Iterative GreenPhyl Orthologous Search Tool) is a fast and user friendly comparative genomic program using a phylogeny-based method to infer orthologs and paralogs in plants. This tools use precomputed phylogeny develops on Oryza sativa and Arabidopsis thaliana full genomes from GreenPhylDB (http://greenphyl.cirad.fr). I-GOST intends to provide a reliable tool for sequence annotation, gene functional analysis or candidate gene search for any plant genome. I-GOST improves time processing performance by using pre calculated phylogenetic analyses available for more than 4000 of validated families from GreenPhylDB database. I-GOST gives clear phylogenetic scores, ranked by bootstrap confidence from a list of plant genes. I-GOST is a publicly accessible tool available on-line (http://greenphyl.cines.fr/cgi-bin/i-gost.cgi)